CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/722,544A

CRF Processing Date: 3/25/2002
Edited by: _____
Verified by: _____ (STIC staff)

ENTERED

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☑ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: 3
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

```
RAW SEQUENCE LISTING              DATE: 03/25/2002
PATENT APPLICATION:  US/09/722,544A    TIME: 12:43:36

Input Set : A:\07334-362001.txt
Output Set: N:\CRF3\03222002\I722544A.raw
```

p.6

```
 3 <110> APPLICANT: Hong, Chen
 4        Freimer, Nelson B.
 6 <120> TITLE OF INVENTION: METHODS OF DIAGNOSING NEUROPSYCHIATRIC DISORDERS
 8 <130> FILE REFERENCE: 07334-362001
10 <140> CURRENT APPLICATION NUMBER: 09/722,544A
11 <141> CURRENT FILING DATE: 2000-11-28
13 <150> PRIOR APPLICATION NUMBER: 09/236,134
14 <151> PRIOR FILING DATE: 1999-01-22
16 <150> PRIOR APPLICATION NUMBER: 60/078,044
17 <151> PRIOR FILING DATE: 1998-03-16
19 <150> PRIOR APPLICATION NUMBER: 60/088,312
20 <151> PRIOR FILING DATE: 1998-06-05
22 <150> PRIOR APPLICATION NUMBER: 60/106,056
23 <151> PRIOR FILING DATE: 1998-10-28
25 <160> NUMBER OF SEQ ID NOS: 33
27 <170> SOFTWARE: FastSEQ for Windows Version 3.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 2055
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (285)...(1769)
38 <400> SEQUENCE: 1
39 tgcgtcacct gcaggcccgg gccgcggggt tggtttccac cctggaggtt gctgacaccc    60
40 tgtgccctcg gctgacttcc agccggtggc acagacgcct ccagggggca gcactcaagc   120
41 gcatcttagg aatgacagag ttgcgtccct ctctgttgcc aggctggagt tcagtggcat   180
42 gttcttagct cactgaagcc tcaaattcct gggttcaagt gaccctccca cctcagcccc   240
43 atgaggacct gggactacag gacacagcta aatccctgac acgg atg aaa att aaa   296
44                                                  Met Lys Ile Lys
45                                                   1
47 gca gag aaa aac gaa ggt cct tcc aga agc tgg tgg caa ctt cac tgg   344
48 Ala Glu Lys Asn Glu Gly Pro Ser Arg Ser Trp Trp Gln Leu His Trp
49  5                  10                  15                  20
51 gga gat att gca aat aac agc ggg aac atg aag ccg cca ctc ttg gtg   392
52 Gly Asp Ile Ala Asn Asn Ser Gly Asn Met Lys Pro Pro Leu Leu Val
53                  25                  30                  35
55 ttt att gtg tgt ctg ctg tgg ttg aaa gac agt cac tgc gca ccc act   440
56 Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Cys Ala Pro Thr
57                  40                  45                  50
59 tgg aag gac aaa act gct atc agt gaa aac ctg aag agt ttt tct gag   488
60 Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe Ser Glu
61          55                  60                  65
```

```
63 gtg ggg gag ata gat gca gat gaa gag gtg aag aag gct ttg act ggt      536
64 Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu Thr Gly
65     70                  75                  80
67 att aag caa atg aaa atc atg atg gaa aga aaa gag aag gaa cac acc      584
68 Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu His Thr
69 85                  90                  95                  100
71 aat cta atg agc acc ctg aag aaa tgc aga gaa gaa aag cag gag gcc      632
72 Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln Glu Ala
73                 105                 110                 115
75 ctg aaa ctt ctg aat gaa gtt caa gaa cat ctg gag gaa gaa gaa agg      680
76 Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu Glu Glu Arg
77                 120                 125                 130
79 cta tgc cgg gag tct ttg gca gat tcc tgg ggt gaa tgc agg tct tgc      728
80 Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg Ser Cys
81                 135                 140                 145
83 ctg gaa aat aac tgc atg aga att tat aca acc tgc caa cct agc tgg      776
84 Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys Gln Pro Ser Trp
85     150                 155                 160
87 tcc tct gtg aaa aat aag att gaa cgg ttt ttc agg aag ata tat caa      824
88 Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg Lys Ile Tyr Gln
89 165                 170                 175                 180
91 ttt cta ttt cct ttc cat gaa gat aat gaa aaa gat ctc ccc atc agt      872
92 Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp Leu Pro Ile Ser
93                 185                 190                 195
95 gaa aag ctc att gag gaa gat gca caa ttg acc caa atg gag gat gtg      920
96 Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln Met Glu Asp Val
97                 200                 205                 210
99 ttc agc cag ttg act gtg gat gtg aat tct ctc ttt aac agg agt ttt      968
100 Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe Asn Arg Ser Phe
101                 215                 220                 225
103 aac gtc ttc aga cag atg cag caa gag ttt gac cag act ttt caa tca      1016
104 Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln Thr Phe Gln Ser
105     230                 235                 240
107 cat ttc ata tca gat aca gac cta act gag cct tac ttt ttt cca gct      1064
108 His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr Phe Phe Pro Ala
109 245                 250                 255                 260
111 ttc tct aaa gag ccg atg aca aaa gca gat ctt gag caa tgt tgg gac      1112
112 Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu Gln Cys Trp Asp
113                 265                 270                 275
115 att ccc aac ttc ttc cag ctg ttt tgt aat ttc agt gtc tct att tat      1160
116 Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser Val Ser Ile Tyr
117                 280                 285                 290
119 gaa agt gtc agt gaa aca att act aag atg ctg aag gca ata gaa gat      1208
120 Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys Ala Ile Glu Asp
121     295                 300                 305
123 tta cca aaa caa gac aaa gct cct gac cac gga ggc ctg att tca aag      1256
124 Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly Leu Ile Ser Lys
125     310                 315                 320
127 atg tta cct ggg cag gac aga gga ctg tgt ggg gaa ctt gac cag aat      1304
```

```
128 Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu Leu Asp Gln Asn
129 325               330           335           Leu Asp Gln   340
131 ttg tca aga tgt ttc aaa ttt cat gaa aaa tgc caa aaa tgt cag gct     1352
132 Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln Lys Cys Gln Ala
133               345           350                       355
135 cac cta tct gaa gac tgt cct gat gta cct gct ctg cac aca gaa tta     1400
136 His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu His Thr Glu Leu
137               360                       365           370
139 gac gag gcg atc agg ttg gtc aat gta tcc aat cag cag tat ggc cag     1448
140 Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln Gln Tyr Gly Gln
141               375                       380           385
143 att ctc cag atg acc cgg aag cac ttg gag gac acc gcc tat ctg gtg     1496
144 Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr Ala Tyr Leu Val
145               390                       395           400
147 gag aag atg aga ggg caa ttt ggc tgg gtg tct gaa ctg gca aac cag     1544
148 Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu Leu Ala Asn Gln
149 405               410                       415           420
151 gcc cca gaa aca gag atc atc ttt aat tca ata cag gta gtt cca agg     1592
152 Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln Val Val Pro Arg
153               425                       430           435
155 att cat gaa gga aat att tcc aaa caa gat gaa aca atg atg aca gac     1640
156 Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met Met Thr Asp
157               440                       445           450
159 tta agc att ctg cct tcc tct aat ttc aca ctc aag atc cct ctt gaa     1688
160 Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys Ile Pro Leu Glu
161               455                       460           465
163 gaa agt gct gag agt tct aac ttc att ggc tac gta gtg gca aaa gct     1736
164 Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val Val Ala Lys Ala
165 470                       475                       480
167 cta cag cat ttt aag gaa cat ttt aaa acc tgg taagaagatc taatgcatcc     1789
168 Leu Gln His Phe Lys Glu His Phe Lys Thr Trp
169 485               490                       495
171 tatatccagt aagtagaatt atctcttcat ctgggacctg gaaatcctga aataaaaaag     1849
172 gataatgcaa taaacacagt tgcaggaaag tatgttagct atatactatg aagtactctt     1909
173 agtttactta tgttgaatgg cttagctatt aatactcaaa ttgagttaaa atgaaaattc     1969
174 ctccttaaaa aatcaaacgt aatatgtatt acatttcatg gtacattagt agttctttgt     2029
175 atattgaata aatactaaat caccta                                          2055
177 <210> SEQ ID NO: 2
178 <211> LENGTH: 495
179 <212> TYPE: PRT
180 <213> ORGANISM: Homo sapiens
182 <400> SEQUENCE: 2
183 Met Lys Ile Lys Ala Glu Lys Asn Glu Gly Pro Ser Arg Ser Trp Trp
184 1               5                       10            15
185 Gln Leu His Trp Gly Asp Ile Ala Asn Asn Ser Gly Asn Met Lys Pro
186               20                        25            30
187 Pro Leu Leu Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His
188               35                        40            45
189 Cys Ala Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys
```

```
190      50                    55                  60
191 Ser Phe Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys
192 65                  70            75                  80
193 Ala Leu Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu
194            85                  90                  95
195 Lys Glu His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu
196            100                 105                 110
197 Lys Gln Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu
198            115                 120                 125
199 Glu Glu Glu Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu
200      130                 135                 140
201 Cys Arg Ser Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys
202 145                 150                 155                 160
203 Gln Pro Ser Trp Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg
204                 165                 170                 175
205 Lys Ile Tyr Gln Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp
206                 180                 185                 190
207 Leu Pro Ile Ser Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln
208                 195                 200                 205
209 Met Glu Asp Val Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe
210      210                 215                 220
211 Asn Arg Ser Phe Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln
212 225                 230                 235                 240
213 Thr Phe Gln Ser His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr
214                 245                 250                 255
215 Phe Phe Pro Ala Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu
216                 260                 265                 270
217 Gln Cys Trp Asp Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser
218            275                 280                 285
219 Val Ser Ile Tyr Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys
220      290                 295                 300
221 Ala Ile Glu Asp Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly
222 305                 310                 315                 320
223 Leu Ile Ser Lys Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu
224                 325                 330                 335
225 Leu Asp Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln
226            340                 345                 350
227 Lys Cys Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu
228            355                 360                 365
229 His Thr Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln
230      370                 375                 380
231 Gln Tyr Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr
232 385                 390                 395                 400
233 Ala Tyr Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu
234                 405                 410                 415
235 Leu Ala Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln
236            420                 425                 430
237 Val Val Pro Arg Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr
238      435                 440                 445
```

```
239 Met Met Thr Asp Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys
240       450                 455                 460
241 Ile Pro Leu Glu Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val
242 465                 470                 475                 480
243 Val Ala Lys Ala Leu Gln His Phe Lys Glu His Phe Lys Thr Trp
244                 485                 490                 495
246 <210> SEQ ID NO: 3
247 <211> LENGTH: 1957
248 <212> TYPE: DNA
249 <213> ORGANISM: Homo sapiens
251 <220> FEATURE:
252 <221> NAME/KEY: CDS
253 <222> LOCATION: (241)...(1671)
255 <400> SEQUENCE: 3
256 tgcgtcacct gcaggcccgg gccgcggggt tggtttccac cctggaggtt gctgacaccc    60
257 tgtgccctcg gctgacttcc agccggtggc acagacgcct ccagggggca gcactcaagc   120
258 gcatcttagg aatgacagag ttgcgtccct ctckgttgcc aggctggagt tcagtggcat   180
259 gttcwtagct cactgaagcc tcaaattcct gggttcaagt gaccctccya cctcagcccc   240
260 atg agg acc tgg gac tac agt aac agc ggg aac atg aag ccg cca ctc    288
261 Met Arg Thr Trp Asp Tyr Ser Asn Ser Gly Asn Met Lys Pro Pro Leu
262 1               5                   10                  15
264 ttg gtg ttt att gtg tgt ctg ctg tgg ttg aaa gac agt cac tgc gca    336
265 Leu Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Cys Ala
266             20                  25                  30
268 ccc act tgg aag gac aaa act gct atc agt gaa aac ctg aag agt ttt    384
269 Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe
270         35                  40                  45
272 tct gag gtg ggg gag ata gat gca gat gaa gag gtg aag aag gct ttg    432
273 Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu
274     50                  55                  60
276 act ggt att aag caa atg aaa atc atg atg gaa aga aaa gag aag gaa    480
277 Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu
278 65                  70                  75                  80
280 cac acc aat cta atg agc acc ctg aag aaa tgc aga gaa gaa aag cag    528
281 His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln
282             85                  90                  95
284 gag gcc ctg aaa ctt ctg aat gaa gtt caa gaa cat ctg gag gaa gaa    576
285 Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu Glu
286             100                 105                 110
288 gaa agg cta tgc cgg gag tct ttg gca gat tcc tgg ggt gaa tgc agg    624
289 Glu Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg
290         115                 120                 125
292 tct tgc ctg gaa aat aac tgc atg aga att tat aca acc tgc caa cct    672
293 Ser Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys Gln Pro
294     130                 135                 140
296 agc tgg tcc tct gtg aaa aat aag att gaa cgg ttt ttc agg aag ata    720
297 Ser Trp Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg Lys Ile
298 145                 150                 155                 160
300 tat caa ttt cta ttt cct ttc cat gaa gat aat gaa aaa gat ctc ccc    768
```

```
RAW SEQUENCE LISTING ERROR SUMMARY     DATE: 03/25/2002
PATENT APPLICATION:  US/09/722,544A    TIME: 12:43:38

Input Set : A:\07334-362001.txt
Output Set: N:\CRF3\03222002\I722544A.raw
```

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:7; N Pos. 14635,14685,29727,29879,29880,29930,29939,29950,29953,41743
Seq#:7; N Pos. 41754,41758,41764,41778,41781,41796,52480,55325,56658,59051
Seq#:7; N Pos. 59067,59070,59073,59093,59146,59148,59149,59151,59172,59178
Seq#:7; N Pos. 72168,72236,72243,72247,72303,72308,72312
```